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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Run on: March 26, 2003, 11:15:29 ; Search time 10203.6 Seconds  
(without alignments) 65.601 Million cell updates/sec

Title: US-10-086-184-1  
Perfect score: 23  
Sequence: 1 aaatcggtccggaggcgaaac 23  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 205640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 774614  
Minimum DB seq length: 0  
Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	GenBmbl:	Result No.	Score	Query Match	Length	DB ID	Description
	1: gb_ba:*	1	15.2	66.1	31	A12130	A12130 Oligonucleo
	2: gb_hg:*	2	15.2	66.1	31	6 100041	100041 Sequence 4
	3: gb_in:*	3	15	65.2	40	6 AR135225	AR135225 Sequence
	4: gb_on:*	4	15	65.2	40	6 AR146721	AR146721 Sequence
	5: gb_ov:*	5	15	65.2	40	6 AR152292	AR152292 Sequence
	6: gb_pt:*	6	15	65.2	40	6 AR157830	AR157830 Sequence
	7: gb_ph:*	7	13.8	60.0	23	6 E26384	E26384 Neuralized
	8: gb_pi:*	8	13.8	60.0	26	6 118509	118509 Sequence 9
	9: gb_pr:*	9	13.8	60.0	33	6 AR15214	AR15214 Sequence
	10: gb_ro:*	10	13.8	60.0	37	6 118507	118507 Sequence 7
	11: gb_stb:*	11	13.4	59.1	29	6 AR139903	AR139903 Sequence
	12: gb_sy:*	12	13.6	59.1	29	6 AR167547	AR167547 Sequence
	13: gb_un:*	13	13.6	59.1	34	6 AR123005	AR123005 Sequence
	14: em_bt:*	14	13.6	59.1	34	6 E16665	E16666 Primer 7/1
	15: em_bt:*	15	13.6	59.1	34	6 E34469	E34469 Method of 1
	16: em_bt:*	16	13.4	59.1	34	6 AX196735	AX196735 Sequence
	17: em_bt:*	17	13.4	58.3	33	6 AX323355	AX323355 Sequence
	18: em_bt:*	18	13.4	58.3	33	6 AX323358	AX323358 Sequence
	19: em_bt:*	19	13.2	57.4	27	6 AR117471	AR117471 Sequence
	20: em_bt:*	20	13.2	57.4	33	6 AR151215	AR151215 Sequence
	21: em_bt:*	21	13.2	57.4	40	6 112505	112505 Sequence 26
	22: em_bt:*	22	13.2	57.4	27	6 AR18892	AR18892 Sequence
	23: em_bt:*	23	13	56.5	27	6 AX104878	AX104878 Sequence
	24: em_bt:*	24	12.8	55.7	17	6 I18510	I18510 Sequence 10
	25: em_bt:*	25	12.8	55.7	23	6 AR110511	AR110511 Sequence
	26: em_bt:*	26	12.8	55.7	23	6 AR137064	AR137064 Sequence
	27: em_bt:*	27	12.8	55.7	27	6 AX103993	AX103993 Sequence
	28: em_bt:*	28	12.8	55.7	27	6 AX103994	AX103994 Sequence
	29: em_bt:*	29	12.8	55.7	27	6 AX104878	AX104878 Sequence
	30: em_bt:*	30	12.8	55.7	27	6 AX355056	AX355056 Sequence
	31: em_bt:*	31	12.8	55.7	27	6 AX355386	AX355386 Sequence
	32: em_bt:*	32	12.8	55.7	30	6 AR151183	AR151183 Sequence
	33: em_bt:*	33	12.8	55.7	30	6 AX431450	AX431450 Sequence
	34: em_bt:*	34	12.6	55.7	30	6 AX280543	AX280543 Sequence
	35: em_bt:*	35	12.6	54.8	30	6 AX280548	AX280548 Sequence
	36: em_bt:*	36	12.6	54.8	35	6 AX382274	AX382274 Sequence
	37: em_bt:*	37	12.6	54.8	35	6 AX382292	AX382292 Sequence
	38: em_bt:*	38	12.4	53.9	25	6 I04752	I04752 Sequence 76
	39: em_bt:*	39	12.4	53.9	31	6 AX248578	AX248578 Sequence
	40: em_bt:*	40	12.4	53.9	38	6 I120827	I120827 Sequence 22
	41: em_bt:*	41	12.4	53.9	38	6 I84578	I84578 Sequence 22
	42: em_bt:*	42	12.4	53.9	39	9 HSA224283	AJ224283 Homo Sapi
	43: em_bt:*	43	12.2	53.0	26	6 A66703	A66703 Sequence 11
	44: em_bt:*	44	12.2	53.0	26	6 AR166214	AR166214 Sequence
	45: em_bt:*	45	12.2	53.0	26	6 AX069193	AX069193 Sequence

## ALIGNMENTS

## RESULT 1

LOCUS A12130 Oligonucleotide PMA5622. 31 bp DNA linear PAT 03-DEC-1993  
DEFINITION  
ACCESSION A12130  
VERSION A12130.1 GI:491282  
KEYWORDS SOURCE ORGANISM  
synthetic construct, artificial sequence's.  
FEATURES Location/Qualifiers  
source 1..31 /organism="Synthetic construct"  
/db\_xref="taxon:36330"  
BASE COUNT 11 a 7 c 9 g 4 t

## ORIGIN

Query Match 66.1%; Score 15.2; DB 6; Length 31;  
 Best Local Similarity 85.0%; Pred. No. 2.3e+04;  
 Matches 17; Conservative 0; Mismatches 3;  
 Indels 0; Gaps 0;

Qy 3 ATCGGCTCCGAGGGGAA 22  
 Db 9 ATCGATCCGATCGGGAA 28

## RESULT 2

LOCUS 100041 31 bp SS-DNA  
 DEFINITION Sequence 4 from Patent US 4918166.  
 ACCESSION 100041  
 VERSION 100041-1 GI:271113

## KEYWORDS

Unknown.

ORGANISM

Unknown.

SOURCE

Unknown.

DEFINITION

Unclassified.

ACCESSION

1 (bases 1 to 40)

VERSION

AR146721.1

KEYWORDS

Unknown.

REFERENCE

Kim,S.Young.

AUTHORS

Nucleic acid molecule encoding abscisic acid responsive

element-binding factor 3

Patent: US 6218521-A 51 17-APR-2001;

Location/Qualifiers

1..40

JOURNAL

PAT 21-MAY-1993

FEATURES

source

/organism="unknown"

BASE COUNT

9 a

11 c

9 g

4 t

ORIGIN

Unknown.

DEFINITION

Unclassified.

ACCESSION

1 (bases 1 to 31)

VERSION

AR146721.1

KEYWORDS

Unknown.

REFERENCE

Kingman,A.J., Kingman,S.M. and Adams,S.B.

AUTHORS

Particular hybrid HIV antigens

TITLE

Patent: US 4918166-A 4 17-APR-1990;

JOURNAL

Oxford Gene Systems Limited; Oxford;

GB;

FEATURES

location/Qualifiers

1..31

/organism="unknown"

BASE COUNT

11 a

7 c

9 g

4 t

ORIGIN

Unknown.

DEFINITION

Best Local Similarity

66.1%;

Score 15.2;

DB 6;

Length 31;

Matches 17;

Conservative

0;

Mismatches

3;

Indels

0;

Gaps

0;

ACCESSION

100041

VERSION

100041-1

KEYWORDS

Unknown.

REFERENCE

Kingman,A.J., Kingman,S.M. and Adams,S.B.

AUTHORS

Particular hybrid HIV antigens

TITLE

Patent: US 4918166-A 4 17-APR-1990;

JOURNAL

Oxford Gene Systems Limited; Oxford;

GB;

FEATURES

location/Qualifiers

1..31

/organism="unknown"

BASE COUNT

11 a

7 c

9 g

4 t

ORIGIN

Unknown.

DEFINITION

Best Local Similarity

65.2%;

Score 15;

DB 6;

Length 40;

Matches 18;

Conservative

0;

Mismatches

5;

Indels

0;

Gaps

0;

ACCESSION

AR135225

VERSION

AR135225.1

KEYWORDS

Unknown.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Kim,S.Young

TITLE

Abasic acid responsive element-binding transcription factors

JOURNAL

Patent: US 6194559-A 51 27-FEB-2001;

FEATURES

location/Qualifiers

1..40

/organism="unknown"

BASE COUNT

11 c

12 g

7 t

1 others

ORIGIN

Unknown.

DEFINITION

Best Local Similarity

65.2%;

Score 15;

DB 6;

Length 40;

Matches 18;

Conservative

0;

Mismatches

5;

Indels

0;

Gaps

0;

ACCESSION

AR135225

VERSION

AR135225.1

KEYWORDS

Unknown.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Kim,S.Young

TITLE

Nucleic acid molecule encoding abscisic acid responsive

element-binding factor 2

JOURNAL

Patent: US 6245905-A 51 12-JUN-2001;

RESULT 4

AR146721

VERSION

AR146721.1

KEYWORDS

Unknown.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Kim,S.Young

TITLE

Nucleic acid molecule encoding abscisic acid responsive

element-binding factor 2

JOURNAL

Patent: US 6245905-A 51 12-JUN-2001;

RESULT 5

AR152292

VERSION

AR152292.1

KEYWORDS

Unknown.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Kim,S.Young

TITLE

Nucleic acid molecule encoding abscisic acid responsive

element-binding factor 4

Patent: US 622461-A 51 15-MAY-2001;

Location/Qualifiers

1..40

JOURNAL

PAT 08-AUG-2001

RESULT 6

AR157830

VERSION

AR157830.1

KEYWORDS

Unknown.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Kim,S.Young

TITLE

Nucleic acid molecule encoding abscisic acid responsive

element-binding factor 2

JOURNAL

PAT 17-OCT-2001

FEATURES	Location/Qualifiers
SOURCE	1. 40 /organism="unknown"
BASE COUNT	9 a 11 c 12 g
ORIGIN	1 others
Query Match	65.2%; Score 15; DB 6; Length 40;
Best Local Similarity	78.3%; Pred. No. 2.8e+04; Indels 0; Gaps 0;
Matches	18; Conservative 0; Mismatches 5;
QY	1 AAATGGCTCGAGGGAAAC 23
Db	2 ATTCGCCTTAAGGGGACAC 24
RESULT 7	
E26314/c	
DEFINITION	E26384
LOCUS	23 bp DNA linear PAT 18-JUN-2001
ACCESSION	E26384
VERSION	E26384_1 GI:13025080
KEYWORDS	JP 199337257-A/11.
SOURCE	unidentified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Moroni, N., Hideo,N., Mitsuhiro,Y. and Hideyuki,S.
TITLE	Neutralized protein, polynucleotide encoding said protein and antibody recognizing said protein.
JOURNAL	JP 199337257-A 11 25-MAY-1999;
COMMENT	SUMITOMO ELECTRIC IND LTD
OS	Unidentified
PN	JP 199337257-A/11
PD	25-MAY-1999
PR	PI MOTOMI NAKADA, HIDEO NAKAMURA, MITSUHIRO YOSHIDA, HIDEYUKI SAWA PC C12N15/09, C07K14/47, C07K16/18, C12P21/02, C12Q1/68, G01N33/53// (C12N15/09, C12R1:91), (C12P21/02, C12R1:19), C12N15/00, CC Strandness; Single; FH Topology: Linear; KEY Location/Qualifiers FT source 1. .23 FEATURES SOURCE
1. .23 /organism="unidentified" /db_xref=Taxon:32644"	
BASE COUNT	2 a 8 c 8 g 5 t
ORIGIN	
Query Match	60.0%; Score 13.8; DB 6; Length 23;
Best Local Similarity	88.2%; Pred. No. 1e+05; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 AAATGGCTCGAGGG 17
Db	2 AAAGGGCTCGAGGG 6
RESULT 8	
I18509/c	
LOCUS	I18509 Sequence 9 from patent US 5496831.
DEFINITION	DNA linear PAT 07-OCT-1996
ACCESSION	I18509
VERSION	I18509_1 GI:1598864
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 37)
AUTHORS	Alexander-Bridges,M.C. and Zhao,H.-F.
TITLE	Inhibition of insulin-induced adiposis
JOURNAL	Patent: US 5496831-A 7 05-MAR-1996;
FEATURES	Location/Qualifiers
SOURCE	1. .37 /organism="unknown"
BASE COUNT	8 a 14 c 5 g 10 t
ORIGIN	
Query Match	60.0%; Score 13.8; DB 6; Length 37;
Best Local Similarity	88.2%; Pred. No. 9.8e+04; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	6 GGCTCGAGGGGGAAA 22
Db	18 GGCTGAGGGGGAAA 2
RESULT 9	
AR151214	
LOCUS	AR151214
DEFINITION	Sequence 40 from patent US 6232061.
ACCESSION	AR151214
VERSION	AR151214_1 GI:15117264
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 33)
AUTHORS	Marchionni,M,Andrew. and Johnson,C.D.
TITLE	Homology cloning
JOURNAL	Patent: US 6232061-A 40 15-MAY-2001;
FEATURES	Location/Qualifiers
SOURCE	1. .33 /organism="unknown"
BASE COUNT	6 a 7 c 9 g 5 t
ORIGIN	
Query Match	60.0%; Score 13.8; DB 6; Length 33;
Best Local Similarity	65.2%; Pred. No. 9.9e+04; Indels 0; Gaps 0;
Matches	15; Conservative 2; Mismatches 6;
QY	1 AAATGGCTCGAGGGAAAC 23
Db	3 ATTCGGATCCGGNACNGGRAY 25
RESULT 10	
I18507/c	
LOCUS	I18507
DEFINITION	Sequence 7 from patent US 5496831.
ACCESSION	I18507
VERSION	I18507_1 GI:1598862
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 37)
AUTHORS	Alexander-Bridges,M.C. and Zhao,H.-F.
TITLE	Inhibition of insulin-induced adiposis
JOURNAL	Patent: US 5496831-A 7 05-MAR-1996;
FEATURES	Location/Qualifiers
SOURCE	1. .37 /organism="unknown"
BASE COUNT	8 a 14 c 5 g 10 t
ORIGIN	
Query Match	60.0%; Score 13.8; DB 6; Length 37;
Best Local Similarity	88.2%; Pred. No. 9.8e+04; Indels 0; Gaps 0;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	6 GGCTCGAGGGGGAAA 22

RESULT 11		DNA	linear	PAT 16-JUN-2001	REFERENCE 1 (bases 1 to 34) Mizunashi, W. Authors TITLE Protein having ethylenediamine-N,N'-disuccinic acid:ethylenediamine lyase activity and gene encoding the same JOURNAL Patent: US 6158940-A 5 02-JAN-2001; Location/Qualifiers
AR139903	AR139903 Sequence 81 from patent US 620716.	DNA	linear	PAT 16-JUN-2001	ACCESSION AR139903 DEFINITION Sequence 81 from patent US 620716. LOCUS AR139903.1 VERSION GI:14482399 KEYWORDS ORGANISM Unknown. SOURCE Unclassified. TITLE Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines PATENT: US 6207416-A 81 27-MAR-2001; FEATURES source BASE COUNT 6 a ORIGIN 10 C 9 g 4 t /organism="unknown"
RESULT 12		DNA	linear	PAT 17-DEC-2001	REFERENCE 1 (bases 1 to 29) Tzarev, S.A., Emerson, S. U. and Purcell, R.H. AUTHORS Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines TITLE JOURNAL Patent: US 6287759-A 81 11-SEP-2001; FEATURES source BASE COUNT 6 a ORIGIN 10 C 9 g 4 t /organism="unknown"
AR167547	AR167547 Sequence 81 from patent US 6287759.	DNA	linear	PAT 17-DEC-2001	ACCESSION AR167547 DEFINITION Sequence 81 from patent US 6287759. LOCUS AR167547.1 VERSION GI:17903333 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 29) Tzarev, S.A., Emerson, S. U. and Purcell, R.H. AUTHORS Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines TITLE JOURNAL Patent: US 6287759-A 81 11-SEP-2001; FEATURES source BASE COUNT 6 a ORIGIN 10 C 9 g 4 t /organism="unknown"
RESULT 13		DNA	linear	PAT 16-MAY-2001	REFERENCE 1 (bases 1 to 34) /organism="unidentified" /ab_xref="taxon:32644" /organism="Artificial sequences". FEATURES source BASE COUNT 5 a ORIGIN 10 C 2 g 7 t 10 others /organism="unidentified" /ab_xref="taxon:32644" /organism="Artificial sequences".
AR123005_c	AR123005 Sequence 5 from patent US 6168940.	DNA	linear	PAT 16-MAY-2001	ACCESSION AR123005_c DEFINITION Sequence 5 from patent US 6168940. LOCUS AR123005_c VERSION AR123005_c KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified.
RESULT 14		DNA	linear	PAT 28-JUL-1999	REFERENCE 1 (bases 1 to 34) Mizunashi, W. Authors TITLE PROTEIN HAVING ETHYLENEDIAMINE-N,N'-DISUCCINIC ACID: ETHYLENEDIAMINE LYASE ACTIVITY AND ITS GENE JOURNAL Patent: JP 1998210984-A/3 COMMENT None OC Artificial sequences. PN JP 1998210984-A/3 PD 11-AUG-1998 PF 28-FEB-1997 PR 29-NOV-1996 PI MIZUNASHI WATARU PC C12N15/09, C07H21/04, C12N1/21, C12N9/88, C12P7/46, (C12N15/09, PC C12R1:01), (C12N1/21, C12R1:19), (C12P7/46, C12R1:19); CC strandness: Single; CC topology: Linear; CC hypothetical: No; FH key FT source FT source FEATURES source BASE COUNT 5 a ORIGIN 10 C 2 g 7 t 10 others /organism="unidentified" /ab_xref="taxon:32644" /organism="Artificial sequences".
AR123005	AR123005 Sequence 22	DNA	linear	PAT 16-MAY-2001	ACCESSION AR123005 DEFINITION Sequence 22 from patent US 6168940. LOCUS AR123005.1 VERSION AR123005.1 KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified.
RESULT 15		DNA	linear	PAT 18-JUN-2001	REFERENCE 1 (bases 1 to 34) /organism="unidentified" /ab_xref="taxon:32644" /organism="Artificial sequences". FEATURES source BASE COUNT 1 a ORIGIN 10 C 2 g 7 t 10 others /organism="unidentified" /ab_xref="taxon:32644" /organism="Artificial sequences".
E34469/c	E34469 Method of inactivating fumarase,	DNA	linear	PAT 18-JUN-2001	ACCESSION E34469/c DEFINITION Method of inactivating fumarase, microorganism obtained therapy and



